## SEQUENCE LISTING

- <110> Alessi, Dario
   Balendran, Anudharan
   Deak, Maria
   Currie, Richard
   Downes, Peter
   Casamayor, Antonio
- <120> Enzyme
- <130> 002.00170
- <140> US 09/937,009
- <141> 2000-03-17
- <150> PCT/GB00/01004
- <151> 2000-03-17
- <150> GB 9906245.7
- <151> 1999-03-19
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  - Phe Asp Tyr Ile Ala Asp Trp Cys 20
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<223> Description of Artificial Sequence:synthetic peptide sequence that interacts with human PRK2 region B

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Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Glu Glu Met Ala Arg Asp 1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys
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<223> Description of Artificial Sequence:synthetic peptide sequence that interacts with human PRK2 region B

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Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Glu Met Phe Gly Asp
1 5 10 15

Phe Asp Tyr Ile Ala Asp Trp Cys 20

<210> 4

<211> 53

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<220>

<223> region A of PRK2

<400> 4

Glu Asp Val Lys Lys His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala 1 5 10 15

Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
20 25 30

Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro 35 40 45

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Ile Leu Thr Pro Pro
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Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe
                                     10
Glu Tyr Ile Asn Pro Leu Leu
             20
<210> 6
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<223> portion of region B of PRK2
<400> 6
Phe Arg Asp Phe Asp Tyr
<210> 7
<211> 23
<212> PRT
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<220>
<223> region of PKC zeta
Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly Phe
                                    10
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Glu Tyr Ile Asn Pro Leu Leu
             20
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Thr Phe Cys Gly Thr Pro Glu Phe Leu
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Phe Glu Gly Phe Glu Tyr
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                 5
                                    10
Leu Met Asp Lys Lys Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly
            20
                                25
Arg Glu Asp Val Ser Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro
         35
                             40
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Ile Leu Thr Pro Pro Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Gln 50 55 60

Glu Met Phe Arg Asp Phe Asp Tyr Ile Ala Asp Trp Cys 65 70 75

<210> 15 <211> 77 <212> PRT <213> Homo sapiens

<223> region of PRK1

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1 5 10 15

Leu Leu Ala Arg Arg Leu Pro Pro Pro Phe Val Pro Thr Leu Ser Gly
20 25 30

Arg Thr Asp Val Ser Asn Phe Asp Glu Glu Phe Thr Gly Glu Ala Pro 35 40 45

Thr Leu Ser Pro Pro Arg Asp Ala Arg Pro Leu Thr Ala Ala Glu Gln 50 60

Ala Ala Phe Leu Asp Phe Asp Phe Val Ala Gly Gly Cys 65 70 75

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1 5 10 15

Val Tyr Glu Lys Lys Leu Ser Pro Pro Phe Lys Pro Gln Val Thr Ser

Glu Thr Asp Thr Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Met Ile 35 40 45

Thr Ile Thr Pro Pro Asp Gln Asp Asp Ser Met Glu Cys Val Asp Ser 50 55 60

Glu Arg Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Thr Ala 65 70 75 80

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1 5 10 15

Leu Leu Ala Arg Lys Val Glu Pro Pro Phe Lys Pro Leu Leu Gln Ser 20 25 30

Glu Glu Asp Val Ser Gln Phe Asp Ser Lys Phe Thr Arg Gln Thr Pro 35 40 45

Val Asp Ser Pro Asp Asp Ser Thr Leu Ser Glu Ser Ala Asn Gln Val
50 55 60

Phe Leu Gly Phe Thr Tyr Val Ala Pro Ser Val 65 70 75

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Met Glu Ile Lys Ser His Val Phe Phe Ser Leu Ile Asn Trp Asp Asp

1 5 10 15

Leu Ile Asn Lys Lys Ile Thr Pro Pro Phe Asn Pro Asn Val Ser Gly
20 25 30

Pro Asn Glu Leu Arg His Phe Asp Pro Glu Phe Thr Glu Glu Pro Val
35 40 45

Pro Asn Ser Ile Gly Lys Ser Pro Asp Ser Val Leu Val Thr Ala Ser 50 55 60

Val Lys Glu Ala Ala Glu Ala Phe Leu Gly Phe Ser Tyr Ala Pro Pro 65 70 75 80

Thr Asp

<210> 19

<211> 76

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<213> Homo sapiens

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<400> 19

Ser Asp Ile Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu 1 5 10 15

Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp 20 25 30

Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val 35 40 45

Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser 50 55 60

Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro Leu Leu 65 70 75

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Val Ser Ile Thr Glu Cys Ala Lys Glu Lys Phe Gly Glu Phe 50 60

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Phe Xaa Xaa Phe Ser Phe
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<213> Homo sapiens
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<223> PKB consensus sequence
<223> residue 6 is a variable amino acid
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Thr Phe Cys Gly Thr Xaa Glu Leu
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<212> PRT
<213> Homo sapiens
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<223> residue 5 is serine or threonine
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<400> 24
Phe Xaa Xaa Phe Xaa Xaa
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<223> residues 1, 4 and 6 are phenylalanine or tyrosine
<220>
<223> residue 5 is a negatively charged amino acid
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Xaa Xaa Xaa Xaa Xaa
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<223> residue 6 is a variable amino acid
<400> 28
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<212> PRT
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<223> C terminal region of PKC zeta
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Phe Glu Gly Phe Glu Tyr
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<223> residues 2 and 3 are variable amino acids
<223> rsidue 5 is serine or threonine
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Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
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                                25
Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
        3.5
                            40
Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
     50
                         55
                                            60
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Leu 65	Gln	His	Ala	Gln	Pro 70	Pro	Pro	Gln	Pro	Arg 75	Lys	Lys	Arg	Pro	Glu 80
Asp	Phe	Lys	Phe	Gly 85	Lys	Ile	Leu	Gly	Glu 90	Gly	Ser	Phe	Ser	Thr 95	Val
Val	Leu	Ala	Arg 100	Glu	Leu	Ala	Thr	Ser 105	Arg	Glu	Tyr	Ala	Ile 110	Lys	Ile
Leu	Glu	Lys 115	Arg	His	Ile	Ile	Lys 120	Glu	Asn	Lys	Val	Pro 125	Tyr	Val	Thr
Arg	Glu 130	Arg	Asp	Val	Met	Ser 135	Arg	Leu	Asp	His	Pro 140	Phe	Phe	Val	Lys
Leu 145	Tyr	Phe	Thr	Phe	Gln 150	Asp	Asp	Glu	Lys	Leu 155	Tyr	Phe	Gly	Leu	Ser 160
Tyr	Ala	Lys	Asn	Gly 165	Glu	Leu	Leu	Lys	Tyr 170	Ile	Arg	Lys	Ile	Gly 175	Ser
Phe	Asp	Glu	Thr 180	Cys	Thr	Arg	Phe	Tyr 185	Thr	Ala	Glu	Ile	Val 190	Ser	Ala
Leu	Glu	Tyr 195	Leu	His	Gly	Lys	Gly 200	Ile	Ile	His	Arg	Asp 205	Leu	Lys	Pro
Glu	Asn 210	Ile	Leu	Leu	Asn	Glu 215	Asp	Met	His	Ile	Gln 220	Ile	Thr	Asp	Phe
Gly 225	Thr	Ala	Lys	Val	Leu 230	Ser	Pro	Glu	Ser	Lys 235	Gln	Ala	Arg	Ala	Asn 240
Ser	Phe	Val	Gly	Thr 245	Ala	Gln	Tyr	Val	Ser 250	Pro	Glu	Leu	Leu	Thr 255	Glu
Lys	Ser	Ala	Cys 260	Lys	Ser	Ser	Asp	Leu 265	Trp	Ala	Leu	Gly	Cys 270	Ile	Ile
Tyr	Gln	Leu 275	Val	Ala	Gly	Leu	Pro 280	Pro	Phe	Arg	Ala	Gly 285	Asn	Glu	Tyr
Leu	Ile 290	Phe	Gln	Lys	Ile	Ile 295	Lys	Leu	Glu	Tyr	Asp 300	Phe	Pro	Glu	Lys
Phe	Phe	Pro	Lys	Ala	Arg 310	Asp	Leu	Val	Glu	Lys 315	Leu	Leu	Val	Leu	Asp

330 325 Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln 345 340 Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp 365 360 Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly 375 Cys Met Gln Val Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser 385 390 395 Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile 405 410 His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu 425 Asp Glu Lys Arg Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp 440 His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp 455 460 Lys Arg Lys Gly Leu Phe Ala Arg Arg Gln Leu Leu Thr Glu 475 465

Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu

Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys 500 505 510

Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly

490

Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro 515 520 525

Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg 530 535 540

Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln 545 550 555

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<213> Homo sapiens

<220>

<223> PRK2 sequence

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Gly Asp Ser Arg Ser Leu Pro Phe Ser Glu Asn Val Ser Ala Val Gln
20 25 30

Lys Leu Asp Phe Ser Asp Thr Met Val Gln Gln Lys Leu Asp Asp Ile 35 40 45

Lys Asp Arg Ile Lys Arg Glu Ile Arg Lys Glu Leu Lys Ile Lys Glu
50 55 60

Gly Ala Glu Asn Leu Arg Lys Val Thr Thr Asp Lys Lys Ser Leu Ala
65 70 75 80

Tyr Val Asp Asn Ile Leu Lys Lys Ser Asn Lys Lys Leu Glu Glu Leu 85 90 95

His His Lys Leu Gln Glu Leu Asn Ala His Ile Val Val Ser Asp Pro 100 105 110

Glu Asp Ile Thr Asp Cys Pro Arg Thr Pro Asp Thr Pro Asn Asn Asp 115 120 125

Pro Arg Cys Ser Thr Ser Asn Asn Arg Leu Lys Ala Leu Gln Lys Gln 130 135 140

Met Tyr Ser Asn Gly Ser Ser Lys Asp Arg Lys Leu His Gly Thr Ala 165 170 175

Gln Gln Leu Leu Gln Asp Ser Lys Thr Lys Ile Glu Val Ile Arg Met 180 185 190

Gln Ile Leu Gln Ala Val Gln Thr Asn Glu Leu Ala Phe Asp Asn Ala 195 200 205

Lys Pro Val Ile Ser Pro Leu Glu Leu Arg Met Glu Glu Leu Arg His 210 215 220 His Phe Arq Ile Glu Phe Ala Val Ala Glu Gly Ala Lys Asn Val Met Lys Leu Gly Ser Gly Lys Val Thr Asp Arg Lys Ala Leu Ser Glu Ala Gln Ala Arg Phe Asn Glu Ser Ser Gln Lys Leu Asp Leu Lys 265 \ Tyr Ser Leu Glu Gln Arg Leu Asn Glu Val Pro Lys Asn His Pro Lys Ser Arg Ile Ile Ile Glu Glu Leu Ser Leu Val Ala Ala Ser Pro Thr Leu Ser Pro Arg Gln Ser Met Ile Ser Thr Gln Asn Gln Tyr Ser Thr Leu Ser Lys Pro Ala Ala Leu Thr Gly Thr Leu Glu Val Arg Leu Met Gly Cys Gln Asp Ile Leu Glu Asn Val Pro Gly Arg Ser Lys Ala Thr Ser Val Ala Leu Pro Gly Trp Ser Pro Ser Glu Thr Arg Ser Ser Phe Met Ser Arg Thr Ser Lys Ser Lys Ser Gly Ser Ser Arg Asn Leu Leu Lys Thr Asp Asp Leu Ser Asn Asp Val Cys Ala Val Leu Lys Leu Asp Asn Thr Val Val Gly Gln Thr Ser Trp Lys Pro Ile Ser Asn Gln Ser Trp Asp Gln Lys Phe Thr Leu Glu Leu Asp Arg Ser Arg Glu Leu Glu Ile Ser Val Tyr Trp Arg Asp Trp Arg Ser Leu Cys Ala Val Lys Phe Leu Arg Leu Glu Asp Phe Leu Asp Asn Gln Arg His Gly Met Cys Leu

Tyr Leu Glu Pro Gln Gly Thr Leu Phe Ala Glu Val Thr Phe Phe Asn

Pro Val Ile Glu Arg Pro Lys Leu Gln Arg Gln Lys Lys Ile Phe Ser Lys Gln Gln Gly Lys Thr Phe Leu Arg Ala Pro Gln Met Asn Ile Asn Ile Ala Thr Trp Gly Arg Leu Val Arg Arg Ala Ile Pro Thr Val Asn His Ser Gly Thr Phe Ser Pro Gln Ala Pro Val Pro Thr Thr Val Pro Val Val Asp Val Arg Ile Pro Gln Leu Ala Pro Pro Ala Ser Asp Ser Thr Val Thr Lys Leu Asp Phe Asp Leu Glu Pro Glu Pro Pro Ala Pro Pro Arg Ala Ser Ser Leu Gly Glu Ile Asp Glu Ser Ser Glu Leu Arg Val Leu Asp Ile Pro Gly Gln Asp Ser Glu Thr Val Phe Asp Ile Gln Asn Asp Arg Asn Ser Ile Leu Pro Lys Ser Gln Ser Glu Tyr Lys Pro Asp Thr Pro Gln Ser Gly Leu Glu Tyr Ser Gly Ile Gln Glu Leu Glu Asp Arg Arg Ser Gln Gln Arg Phe Gln Phe Asn Leu Gln Asp Phe Arg Cys Cys Ala Val Leu Gly Arg Gly His Phe Gly Lys Val Leu Leu Ala Glu Tyr Lys Asn Thr Asn Glu Met Phe Ala Ile Lys Ala Leu Lys Lys Gly Asp Ile Val Ala Arg Asp Glu Val Asp Ser Leu Met Cys Glu Lys Arg Ile Phe Glu Thr Val Asn Ser Val Arg His Pro Phe Leu 

Val Asn Leu Phe Ala Cys Phe Gln Thr Lys Glu His Val Cys Phe Val

- Met Glu Tyr Ala Ala Gly Gly Asp Leu Met Met His Ile His Thr Asp 740 745 750
- Val Phe Ser Glu Pro Arg Ala Val Phe Tyr Ala Ala Cys Val Val Leu
  755 760 765
- Gly Leu Gln Tyr Leu His Glu His Lys Ile Val Tyr Arg Asp Leu Lys
  770 780
- Leu Asp Asn Leu Leu Leu Asp Thr Glu Gly Phe Val Lys Ile Ala Asp 785 790 795 800
- Phe Gly Leu Cys Lys Glu Gly Met Gly Tyr Gly Asp Arg Thr Ser Thr 805 810 815
- Phe Cys Gly Thr Pro Glu Phe Leu Ala Pro Glu Val Leu Thr Glu Thr 820 825 830
- Ser Tyr Thr Arg Ala Val Asp Trp Trp Gly Leu Gly Val Leu Ile Tyr 835 840 845
- Glu Met Leu Val Gly Glu Ser Pro Phe Pro Gly Asp Asp Glu Glu Glu 850 855 860
- Val Phe Asp Ser Ile Val Asn Asp Glu Val Arg Tyr Pro Arg Phe Leu 865 870 875 880
- Ser Thr Glu Ala Ile Ser Ile Met Arg Arg Leu Leu Arg Arg Asn Pro 885 890 895
- Glu Arg Arg Leu Gly Ala Ser Glu Lys Asp Ala Glu Asp Val Lys Lys
  900 905 910
- His Pro Phe Phe Arg Leu Ile Asp Trp Ser Ala Leu Met Asp Lys Lys 915 920 925
- Val Lys Pro Pro Phe Ile Pro Thr Ile Arg Gly Arg Glu Asp Val Ser 930 935 940
- Asn Phe Asp Asp Glu Phe Thr Ser Glu Ala Pro Ile Leu Thr Pro Pro 945 950 955 960
- Arg Glu Pro Arg Ile Leu Ser Glu Glu Glu Glu Met Phe Arg Asp
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- Phe Asp Tyr Ile Ala Asp Trp Cys 980

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<212> PRT

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Glu Leu Lys Leu Lys Glu Gly Ala Glu Asn Leu Arg Arg Ala Thr Thr 50 55 60

Asp Leu Gly Arg Ser Leu Gly Pro Val Glu Leu Leu Leu Arg Gly Ser
65 70 75 80

Ser Arg Arg Leu Asp Leu Leu His Gln Gln Leu Gln Glu Leu His Ala 85 90 95

His Val Val Leu Pro Asp Pro Ala Ala Thr His Asp Gly Pro Gln Ser 100 105 110

Pro Gly Ala Gly Gly Pro Thr Cys Ser Ala Thr Asn Leu Ser Arg Val

Ala Gly Leu Glu Lys Gln Leu Ala Ile Glu Leu Lys Val Lys Gln Gly 130 135 140

Lys Leu Leu Thr Ala Gln Gln Met Leu Gln Asp Ser Lys Thr Lys 165 170 175

Ile Asp Ile Ile Arg Met Gln Leu Arg Arg Ala Leu Gln Ala Asp Gln
180 185 190

Leu Glu Asn Gln Ala Ala Pro Asp Asp Thr Gln Gly Ser Pro Asp Leu

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Ala	Ala	Lys	Ala	Pro 245	Asp	Arg	Lys	Ala	Val 250	Ser	Glu	Ala	Gln	Glu 255	Lys
Leu	Thr	Glu	Ser 260	Asn	Gln	Lys	Leu	Gly 265	Leu	Leu	Arg	Glu	Ala 270	Leu	Glu
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Arg	Glu 290	Glu	Leu	Ala	Ala	Ala 295	Ser	Ser	Ala	Ala	Phe 300	Ser	Thr	Arg	Leu
Ala 305	Gly	Pro	Phe	Pro	Ala 310	Thr	His	Tyr	Ser	Thr 315	Leu	Сув	Lys	Pro	Ala 320
Pro	Leu	Thr	Gly	Thr 325	Leu	Glu	Val	Arg	Val 330	Val	Gly	Cys	Arg	Asp 335	Leu
Pro	Glu	Thr	Ile 340	Pro	Trp	Asn	Pro	Thr 345	Pro	Ser	Met	Gly	Gly 350	Pro	Gly
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_	370				Ser	375					380				
385					Glu 390					395					400
		-		405	Ser				410					415	
			420		Glu			425					430		
		435			Gln		440					445			
Len	Glu	Asp	Phe	Len	Asp	Asn	Glu	Ara	His	Glu	Val	Gln	Leu	Asp	Met

	450				-	455					460				
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Ile	Glu	Arg	Ile	Pro 485	Arg	Leu	Arg	Arg	Gln 490	Lys	Lys	Ile	Phe	Ser 495	Lys
Gln	Gln	Gly	Lys 500	Ala	Phe	Gln	Arg	Ala 505	Arg	Gln	Met	Asn	Ile 510	Asp	Val
Ala	Thr	Trp 515	Val	Arg	Leu	Leu	Arg 520	Arg	Leu	Ile	Pro	Asn 525	Ala	Thr	Gly
Thr	Gly 530	Thr	Phe	Ser	Pro	Gly 535	Ala	Ser	Pro	Gly	Ser 540	Glu	Ala	Arg	Thr
Thr 545	Gly	Asp	Ile	Ser	Val 550	Glu	Lys	Leu	Asn	Leu 555	Gly	Thr	Asp	Ser	Asp 560
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Leu	Ser	Ser	Pro 580	Ile	Gln	Glu	Ser	Thr 585	Ala	Pro	Glu	Leu	Pro 590	Ser	Glu
Thr	Gln	Glu 595	Thr	Pro	Gly	Pro	Ala 600	Leu	Cys	Ser	Pro	Leu 605	Arg	TÀ2	Ser
Pro	Leu 610	Thr	Leu	Glu	Asp	Phe 615	Lys	Phe	Leu	Ala	Val 620	Leu	Gly	Arg	Gly
His 625	Phe	Gly	Lys	Val	Leu 630	Leu	Ser	Glu	Phe	Arg 635	Pro	Ser	Gly	Glu	Leu 640
Phe	Ala	Ile	Lys	Ala 645	Leu	Lys	Lys	Gly	Asp 650	Ile	Val	Ala	Arg	Asp 655	Glu
Val	Glu	Ser	Leu 660	Met	Cys	Glu	Lys	Arg 665	Ile	Leu	Ala	Ala	Val 670	Thr	Ser
Ala	Gly	His 675	Pro	Phe	Leu	Val	Asn 680	Leu	Phe	Gly	Суз	Phe 685	Gln	Thr	Pro
Glu	His 690	Val	Cys	Phe	Val	Met 695	Glu	Tyr	Ser	Ala	Gly 700	Gly	Asp	Leu	Met
Leu	His	Ile	His	Ser	Asp	Val	Phe	Ser	Glu	Pro	Arg	Ala	Ile	Phe	Tyr

705					710					715					720
Ser	Ala	Cys	Val	Val 725	Leu	Gly	Leu	Gln	Phe 730	Leu	His	Glu	His	Lys 735	Ile
Val	Tyr	Arg	Asp 740	Leu	Lys	Leu	Asp	Asn 745	Leu	Leu	Leu	Asp	Thr 750	Glu	Gly
Tyr	Val	Lys 755	Ile	Ala	Asp	Phe	Gly 760	Leu	Cys	Lys	Glu	Gly 765	Met	Gly	Tyr
Gly	Asp 770	Arg	Thr	Ser	Thr	Phe 775	Cys	Gly	Thr	Pro	Glu 780	Phe	Leu	Ala	Pro
Glu 785	Val	Leu	Thr	Asp	Thr 790	Ser	Tyr	Thr	Arg	Ala 795	Val	Asp	Trp	Trp	800
Leu	Gly	Val	Leu	Leu 805	Tyr	Glu	Met	Leu	Val 810	Gly	Glu	Ser	Pro	Phe 815	Pro
Gly	Asp	Asp	Glu 820	Glu	Glu	Val	Phe	Asp 825	Ser	Ile	Val	Asn	Asp 830	Glu	Val
Arg	Tyr	Pro 835	Arg	Phe	Leu	Ser	Ala 840	Glu	Ala	Ile	Gly	Ile 845	Met	Arg	Arg
Leu	Leu 850	Arg	Arg	Asn	Pro	Glu 855	Arg	Arg	Leu	Gly	Ser 860	Ser	Glu	Arg	Asp
Ala 865	Glu	Asp	Val	Lys	Lys 870	Gln	Pro	Phe	Phe	Arg 875	Thr	Leu	Gly	Trp	Glu 880
Ala	Leu	Leu	Ala	Arg 885	Arg	Leu	Pro	Pro	Pro 890	Phe	Val	Pro	Thr	Leu 895	Ser
Gly	Arg	Thr	Asp 900	Val	Ser	Asn	Phe	Asp 905	Glu	Glu	Phe	Thr	Gly 910	Glu	Ala
Pro	Thr	Leu 915	Ser	Pro	Pro	Arg	Asp 920	Ala	Arg	Pro	Leu	Thr 925	Ala	Ala	Glu
Gln	Ala 930	Ala	Phe	Leu	Asp	Phe 935	Asp	Phe	Val	Ala	Gly 940	Gly	Cys		

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<211> 592

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<213> Homo sapiens

<220>

<223> PKC zeta sequence

<400> 34

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Arg Leu Lys Ala His Tyr Gly Gly Asp Ile Phe Ile Thr Ser Val Asp
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Ala Ala Thr Thr Phe Glu Glu Leu Cys Glu Glu Val Arg Asp Met Cys
35 40 45

Arg Leu His Gln Gln His Pro Leu Thr Leu Lys Trp Val Asp Ser Glu 50 55 60

Gly Asp Pro Cys Thr Val Ser Ser Gln Met Glu Leu Glu Glu Ala Phe
65 70 75 80

Arg Leu Ala Arg Gln Cys Arg Asp Glu Gly Leu Ile Ile His Val Phe 85 90 95

Pro Ser Thr Pro Glu Gln Pro Gly Leu Pro Cys Pro Gly Glu Asp Lys
100 105 110

Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Arg Ala 115 120 125

Asn Gly His Leu Phe Gln Ala Lys Arg Phe Asn Arg Arg Ala Tyr Cys 130 135 140

Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu Ala Arg Gln Gly Tyr Arg 145 150 155 160

Cys Ile Asn Cys Lys Leu Leu Val His Lys Arg Cys His Gly Leu Val 165 170 175

Pro Leu Thr Cys Arg Lys His Met Asp Ser Val Met Pro Ser Gln Glu 180 185 190

Pro Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu
195 200 205

Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile 210 215 220 Lys Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Thr Tyr Ala Lys Val Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe 

- Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp 485 490 495
- Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile 500 505 510
- Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys 515 520 525
- Lys Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly 530 535 540
- Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr 545 550 555 555
- Pro Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu 565 570 575
- Gly Phe Glu Tyr Ile Asn Pro Leu Leu Ser Thr Glu Glu Ser Val 580 585 590